SEQUENCE LISTING

<110> Nakamura, Yusuke
      Nakagawa, Hidewaki
      Nakatsuru, Shuichi

<120> EphA4 AS THERAPEUTIC TARGET OF PRC AND
   PDACa

<130> 082368-009500US

<150> PCT/JP2005/003081
<151> 2005-02-18

<150> US 60/555,809
<151> 2004-03-24

<150> US 60/548,335
<151> 2004-02-27

<160> 23

<170> PatentIn version 3.1

<210> 1
<211> 3468
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (43)..(3003)
<223>

<400> 1
ctgggataga agcggcagga gcagcgttgg caccggcgaa cc atg gct ggg att   54
                                               Met Ala Gly Ile
                                               1

ttc tat ttc gcc cta ttt tcg tgt ctc ttc ggg att tgc gac gct gtc   102
Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile Cys Asp Ala Val
5   10   15   20

aca ggt tcc agg gta tac ccc gcg aat gaa gtt acc tta ttg gat tcc   150
Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr Leu Leu Asp Ser
                25   30   35

aga tct gtt cag gga gaa ctt ggg tgg ata gca agc cct ctg gaa gga   198
Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser Pro Leu Glu Gly
            40   45   50

ggg tgg gag gaa gtg agt atc atg gat gaa aaa aat aca cca atc cga   246
Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn Thr Pro Ile Arg
        55   60   65

acc tac caa gtg tgc aat gtg atg gaa ccc agc cag aat aac tgg cta   294
Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln Asn Asn Trp Leu
        70   75   80

cga act gat tgg atc acc cga gaa ggg gct cag agg gtg tat att gag   342

```
Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg Val Tyr Ile Glu
85              90              95              100

att aaa ttc acc ttg agg gac tgc aat agt ctt ccg ggc gtc atg ggg    390
Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro Gly Val Met Gly
            105             110             115

act tgc aag gag acg ttt aac ctg tac tac tat gaa tca gac aac gac    438
Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu Ser Asp Asn Asp
            120             125             130

aaa gag cgt ttc atc aga gag aac cag ttt gtc aaa att gac acc att    486
Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys Ile Asp Thr Ile
            135             140             145

gct gct gat gag agc ttc acc caa gtg gac att ggt gac aga atc atg    534
Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly Asp Arg Ile Met
            150             155             160

aag ctg aac acc gag atc cgg gat gta ggg cca tta agc aaa aag ggg    582
Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu Ser Lys Lys Gly
165             170             175             180

ttt tac ctg gct ttt cag gat gtg ggg gcc tgc atc gcc ctg gta tca    630
Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile Ala Leu Val Ser
            185             190             195

gtc cgt gtg ttc tat aaa aag tgt cca ctc aca gtc cgc aat ctg gcc    678
Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val Arg Asn Leu Ala
            200             205             210

cag ttt cct gac acc atc aca ggg gct gat acg tct tcc ctg gtg gaa    726
Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser Ser Leu Val Glu
            215             220             225

gtt cga ggc tcc tgt gtc aac aac tca gaa gag aaa gat gtg cca aaa    774
Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys Asp Val Pro Lys
            230             235             240

atg tac tgt ggg gca gat ggt gaa tgg ctg gta ccc att ggc aac tgc    822
Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro Ile Gly Asn Cys
245             250             255             260

cta tgc aac gct ggg cat gag gag cgg agc gga gaa tgc caa gct tgc    870
Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu Cys Gln Ala Cys
                265             270             275

aaa att gga tat tac aag gct ctc tcc acg gat gcc acc tgt gcc aag    918
Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala Thr Cys Ala Lys
            280             285             290

tgc cca ccc cac agc tac tct gtc tgg gaa gga gcc acc tcg tgc acc    966
Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala Thr Ser Cys Thr
            295             300             305

tgt gac cga ggc ttt ttc aga gct gac aac gat gct gcc tct atg ccc    1014
Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala Ala Ser Met Pro
310             315             320

tgc acc cgt cca cca tct gct ccc ctg aac ttg att tca aat gtc aac    1062
Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile Ser Asn Val Asn
```

2

```
gag aca tct gtg aac ttg gaa tgg agt agc cct cag aat aca ggt ggc      1110
Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln Asn Thr Gly Gly
                345                 350                 355

cgc cag gac att tcc tat aat gtg gta tgc aag aaa tgt gga gct ggt      1158
Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys Cys Gly Ala Gly
            360                 365                 370

gac ccc agc aag tgc cga ccc tgt gga agt ggg gtc cac tac acc cca      1206
Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val His Tyr Thr Pro
            375                 380                 385

cag cag aat ggc ttg aag acc acc aaa gtc tcc atc act gac ctc cta      1254
Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile Thr Asp Leu Leu
            390                 395                 400

gct cat acc aat tac acc ttt gaa atc tgg gct gtg aat gga gtg tcc      1302
Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val Asn Gly Val Ser
405                 410                 415                 420

aaa tat aac cct aac cca gac caa tca gtt tct gtc act gtg acc acc      1350
Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val Thr Val Thr Thr
                425                 430                 435

aac caa gca gca cca tca tcc att gct ttg gtc cag gct aaa gaa gtc      1398
Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln Ala Lys Glu Val
                440                 445                 450

aca aga tac agt gtg gca ctg gct tgg ctg gaa cca gat cgg ccc aat      1446
Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro Asp Arg Pro Asn
            455                 460                 465

ggg gta atc ctg gaa tat gaa gtc aag tat tat gag aag gat cag aat      1494
Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu Lys Asp Gln Asn
            470                 475                 480

gag cga agc tat cgt ata gtt cgg aca gct gcc agg aac aca gat atc      1542
Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg Asn Thr Asp Ile
485                 490                 495                 500

aaa ggc ctg aac cct ctc act tcc tat gtt ttc cac gtg cga gcc agg      1590
Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His Val Arg Ala Arg
                505                 510                 515

aca gca gct ggc tat gga gac ttc agt gag ccc ttg gag gtt aca acc      1638
Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu Glu Val Thr Thr
            520                 525                 530

aac aca gtg cct tcc cgg atc att gga gat ggg gct aac tcc aca gtc      1686
Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala Asn Ser Thr Val
            535                 540                 545

ctt ctg gtc tct gtc tcg ggc agt gtg gtg ctg gtg gta att ctc att      1734
Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val Val Ile Leu Ile
            550                 555                 560

gca gct ttt gtc atc agc cgg aga cgg agt aaa tac agt aaa gcc aaa      1782
Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr Ser Lys Ala Lys
565                 570                 575                 580
```

3

```
caa gaa gcg gat gaa gag aaa cat ttg aat caa ggt gta aga aca tat       1830
Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly Val Arg Thr Tyr
                585                     590                     595

gtg gac ccc ttt acg tac gaa gat ccc aac caa gca gtg cga gag ttt       1878
Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala Val Arg Glu Phe
                600                     605                     610

gcc aaa gaa att gac gca tcc tgc att aag att gaa aaa gtt ata gga       1926
Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu Lys Val Ile Gly
                615                     620                     625

gtt ggt gaa ttt ggt gag gta tgc agt ggg cgt ctc aaa gtg cct ggc       1974
Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Val Pro Gly
    630                     635                     640

aag aga gag atc tgt gtg gct atc aag act ctg aaa gct ggt tat aca       2022
Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr
645     .               650                     655                 660

gac aaa cag agg aga gac ttc ctg agt gag gcc agc atc atg gga cag       2070
Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser Ile Met Gly Gln
                665                     670                     675

ttt gac cat ccg aac atc att cac ttg gaa ggc gtg gtc act aaa tgt       2118
Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val Val Thr Lys Cys
                680                     685                     690

aaa cca gta atg atc ata aca gag tac atg gag aat ggc tcc ttg gat       2166
Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn Gly Ser Leu Asp
                695                     700                     705

gca ttc ctc agg aaa aat gat ggc aga ttt aca gtc att cag ctg gtg       2214
Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val Ile Gln Leu Val
                710                     715                     720

ggc atg ctt cgt ggc att ggg tct ggg atg aag tat tta tct gat atg       2262
Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr Leu Ser Asp Met
725                     730                     735                 740

agc tat gtg cat cgt gat ctg gcc gca cgg aac atc ctg gtg aac agc       2310
Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser
                745                     750                     755

aac ttg gtc tgc aaa gtg tct gat ttt ggc atg tcc cga gtg ctt gag       2358
Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser Arg Val Leu Glu
                760                     765                     770

gat gat ccg gaa gca gct tac acc acc agg ggt ggc aag att cct atc       2406
Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly Lys Ile Pro Ile
                775                     780                     785

cgg tgg act gcg cca gaa gca att gcc tat cgt aaa ttc aca tca gca       2454
Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys Phe Thr Ser Ala
    790                     795                     800

agt gat gta tgg agc tat gga atc gtt atg tgg gaa gtg atg tcg tac       2502
Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu Val Met Ser Tyr
805                     810                     815                 820
```

4

```
ggg gag agg ccc tat tgg gat atg tcc aat caa gat gtg att aaa gcc        2550
Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp Val Ile Lys Ala
            825             830             835

att gag gaa ggc tat cgg tta ccc cct cca atg gac tgc ccc att gcg        2598
Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp Cys Pro Ile Ala
            840             845             850

ctc cac cag ctg atg cta gac tgc tgg cag aag gag agg agc gac agg        2646
Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu Arg Ser Asp Arg
            855             860             865

cct aaa ttt ggg cag att gtc aac atg ttg gac aaa ctc atc cgc aac        2694
Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys Leu Ile Arg Asn
        870             875             880

ccc aac agc ttg aag agg aca ggg acg gag agc tcc aga cct aac act        2742
Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser Arg Pro Asn Thr
885             890             895             900

gcc ttg ttg gat cca agc tcc cct gaa ttc tct gct gtg gta tca gtg        2790
Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala Val Val Ser Val
            905             910             915

ggc gat tgg ctc cag gcc att aaa atg gac cgg tat aag gat aac ttc        2838
Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr Lys Asp Asn Phe
            920             925             930

aca gct gct ggt tat acc aca cta gag gct gtg gtg cac gtg aac cag        2886
Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val His Val Asn Gln
            935             940             945

gag gac ctg gca aga att ggt atc aca gcc atc acg cac cag aat aag        2934
Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr His Gln Asn Lys
        950             955             960

att ttg agc agt gtc cag gca atg cga acc caa atg cag cag atg cac        2982
Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met Gln Gln Met His
965             970             975             980

ggc aga atg gtt ccc gtc tga gccagtactg aataaactca aaactcttga          3033
Gly Arg Met Val Pro Val
            985

aattagttta cctcatccat gcactttaat tgaagaactg cacttttttt acttcgtctt     3093
cgccctctga aattaaagaa atgaaaaaaa aaaacaatat ctgcagcgtt gcttggtgca     3153
cagattgctg aaactgtggg gcttacagaa atgactgccg gtcatttgaa tgagacctgg     3213
aacaaatcgt ttctcagaag tacttttctg ttcatcacca gtctgtaaaa tacatgtacc     3273
tatagaaata gaacactgcc tctgagtttt gatgctgtat ttgctgccag acactgagct     3333
tctgagacat ccctgattct ctctccattt ggaattacaa ccattgtatt ttgtttgtgg     3393
cataaattac agtcatctgt ctttcactgg aatgaagacc atgcctagga acattttta      3453
aggactcagc tgtgg                                                       3468


<210>   2
<211>   986
<212>   PRT
<213>   Homo sapiens

<400>   2
Met Ala Gly Ile Phe Tyr Phe Ala Leu Phe Ser Cys Leu Phe Gly Ile
```

5

```
        1                5                        10                         15

     Cys Asp Ala Val Thr Gly Ser Arg Val Tyr Pro Ala Asn Glu Val Thr
                 20               25               30

     Leu Leu Asp Ser Arg Ser Val Gln Gly Glu Leu Gly Trp Ile Ala Ser
             35               40               45

     Pro Leu Glu Gly Gly Trp Glu Glu Val Ser Ile Met Asp Glu Lys Asn
         50               55               60

     Thr Pro Ile Arg Thr Tyr Gln Val Cys Asn Val Met Glu Pro Ser Gln
     65               70               75               80

     Asn Asn Trp Leu Arg Thr Asp Trp Ile Thr Arg Glu Gly Ala Gln Arg
                 85               90               95

     Val Tyr Ile Glu Ile Lys Phe Thr Leu Arg Asp Cys Asn Ser Leu Pro
                 100              105              110

     Gly Val Met Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr Tyr Glu
                 115              120              125

     Ser Asp Asn Asp Lys Glu Arg Phe Ile Arg Glu Asn Gln Phe Val Lys
         130              135              140

     Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Val Asp Ile Gly
     145              150              155              160

     Asp Arg Ile Met Lys Leu Asn Thr Glu Ile Arg Asp Val Gly Pro Leu
                 165              170              175

     Ser Lys Lys Gly Phe Tyr Leu Ala Phe Gln Asp Val Gly Ala Cys Ile
                 180              185              190

     Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Leu Thr Val
                 195              200              205

     Arg Asn Leu Ala Gln Phe Pro Asp Thr Ile Thr Gly Ala Asp Thr Ser
         210              215              220

     Ser Leu Val Glu Val Arg Gly Ser Cys Val Asn Asn Ser Glu Glu Lys
     225              230              235              240

     Asp Val Pro Lys Met Tyr Cys Gly Ala Asp Gly Glu Trp Leu Val Pro
                 245              250              255

     Ile Gly Asn Cys Leu Cys Asn Ala Gly His Glu Glu Arg Ser Gly Glu
                 260              265              270

     Cys Gln Ala Cys Lys Ile Gly Tyr Tyr Lys Ala Leu Ser Thr Asp Ala
             275              280              285

     Thr Cys Ala Lys Cys Pro Pro His Ser Tyr Ser Val Trp Glu Gly Ala
         290              295              300

     Thr Ser Cys Thr Cys Asp Arg Gly Phe Phe Arg Ala Asp Asn Asp Ala
     305              310              315              320

     Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala Pro Leu Asn Leu Ile


                                    6
```

```
                    325                     330                     335
Ser Asn Val Asn Glu Thr Ser Val Asn Leu Glu Trp Ser Ser Pro Gln
            340                 345                 350

Asn Thr Gly Gly Arg Gln Asp Ile Ser Tyr Asn Val Val Cys Lys Lys
            355                 360                 365

Cys Gly Ala Gly Asp Pro Ser Lys Cys Arg Pro Cys Gly Ser Gly Val
            370                 375                 380


His Tyr Thr Pro Gln Gln Asn Gly Leu Lys Thr Thr Lys Val Ser Ile
385                 390                 395                 400

Thr Asp Leu Leu Ala His Thr Asn Tyr Thr Phe Glu Ile Trp Ala Val
                405                 410                 415

Asn Gly Val Ser Lys Tyr Asn Pro Asn Pro Asp Gln Ser Val Ser Val
                420                 425                 430

Thr Val Thr Thr Asn Gln Ala Ala Pro Ser Ser Ile Ala Leu Val Gln
            435                 440                 445

Ala Lys Glu Val Thr Arg Tyr Ser Val Ala Leu Ala Trp Leu Glu Pro
    450                 455                 460

Asp Arg Pro Asn Gly Val Ile Leu Glu Tyr Glu Val Lys Tyr Tyr Glu
465                 470                 475                 480

Lys Asp Gln Asn Glu Arg Ser Tyr Arg Ile Val Arg Thr Ala Ala Arg
                485                 490                 495

Asn Thr Asp Ile Lys Gly Leu Asn Pro Leu Thr Ser Tyr Val Phe His
                500                 505                 510

Val Arg Ala Arg Thr Ala Ala Gly Tyr Gly Asp Phe Ser Glu Pro Leu
            515                 520                 525

Glu Val Thr Thr Asn Thr Val Pro Ser Arg Ile Ile Gly Asp Gly Ala
    530                 535                 540

Asn Ser Thr Val Leu Leu Val Ser Val Ser Gly Ser Val Val Leu Val
545                 550                 555                 560

Val Ile Leu Ile Ala Ala Phe Val Ile Ser Arg Arg Arg Ser Lys Tyr
                565                 570                 575

Ser Lys Ala Lys Gln Glu Ala Asp Glu Glu Lys His Leu Asn Gln Gly
            580                 585                 590

Val Arg Thr Tyr Val Asp Pro Phe Thr Tyr Glu Asp Pro Asn Gln Ala
            595                 600                 605

Val Arg Glu Phe Ala Lys Glu Ile Asp Ala Ser Cys Ile Lys Ile Glu
    610                 615                 620

Lys Val Ile Gly Val Gly Glu Phe Gly Glu Val Cys Ser Gly Arg Leu
625                 630                 635                 640

Lys Val Pro Gly Lys Arg Glu Ile Cys Val Ala Ile Lys Thr Leu Lys


                                7
```

Ala Gly Tyr Thr Asp Lys Gln Arg Arg Asp Phe Leu Ser Glu Ala Ser
        660   665   670

Ile Met Gly Gln Phe Asp His Pro Asn Ile Ile His Leu Glu Gly Val
        675   680   685

Val Thr Lys Cys Lys Pro Val Met Ile Ile Thr Glu Tyr Met Glu Asn
    690   695   700

Gly Ser Leu Asp Ala Phe Leu Arg Lys Asn Asp Gly Arg Phe Thr Val
705   710   715   720

Ile Gln Leu Val Gly Met Leu Arg Gly Ile Gly Ser Gly Met Lys Tyr
            725   730   735

Leu Ser Asp Met Ser Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
        740   745   750

Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Met Ser
        755   760   765

Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr Arg Gly Gly
    770   775   780

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ala Tyr Arg Lys
785   790   795   800

Phe Thr Ser Ala Ser Asp Val Trp Ser Tyr Gly Ile Val Met Trp Glu
            805   810   815

Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Asp Met Ser Asn Gln Asp
        820   825   830

Val Ile Lys Ala Ile Glu Glu Gly Tyr Arg Leu Pro Pro Pro Met Asp
        835   840   845

Cys Pro Ile Ala Leu His Gln Leu Met Leu Asp Cys Trp Gln Lys Glu
    850   855   860

Arg Ser Asp Arg Pro Lys Phe Gly Gln Ile Val Asn Met Leu Asp Lys
865   870   875   880

Leu Ile Arg Asn Pro Asn Ser Leu Lys Arg Thr Gly Thr Glu Ser Ser
            885   890   895

Arg Pro Asn Thr Ala Leu Leu Asp Pro Ser Ser Pro Glu Phe Ser Ala
        900   905   910

Val Val Ser Val Gly Asp Trp Leu Gln Ala Ile Lys Met Asp Arg Tyr
        915   920   925

Lys Asp Asn Phe Thr Ala Ala Gly Tyr Thr Thr Leu Glu Ala Val Val
    930   935   940

His Val Asn Gln Glu Asp Leu Ala Arg Ile Gly Ile Thr Ala Ile Thr
945   950   955   960

His Gln Asn Lys Ile Leu Ser Ser Val Gln Ala Met Arg Thr Gln Met
            965   970   975

8

Gln Gln Met His Gly Arg Met Val Pro Val
          980   985

<210> 3
<211> 23
<212> DNA
<213> Artificial

<220>
<223> An artificial synthesized primer sequence for RT-PCR

<400> 3
gaaggcgtgg tcactaaatg taa   23

<210> 4
<211> 22
<212> DNA
<213> Artificial

<220>
<223> An artificial synthesized primer sequence for RT-PCR

<400> 4
tttaatttca gagggcgaag ac   22

<210> 5
<211> 23
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence for RT-PCR

<400> 5
catccacgaa actaccttca act   23

<210> 6
<211> 23
<212> DNA
<213> Artificial

<220>
<223> An artificially synthesized primer sequence for RT-PCR

<400> 6
tctccttaga gagaagtggg gtg   23

<210> 7
<211> 20
<212> DNA
<213> Artificial

<220>
<223> An artificial synthesized primer sequence for RT-PCR

9

```
<400>  7
caccccact gaaaaagaga                                              20


<210>  8
<211>  19
<212>  DNA
<213>  Artificial

<220>
<223>  An artificial synthesized primer sequence for RT-PCR

<400>  8
tacctgtgga gcaaggtgc                                              19


<210>  9
<211>  9
<212>  DNA
<213>  Artificial

<220>
<223>  An artificially synthesized spcer sequence for siRNA

<400>  9
ttcaagaga                                                         9


<210>  10
<211>  19
<212>  DNA
<213>  Artificial

<220>
<223>  An artificial synthesized target sequence for siRNA

<400>  10
gcagcaccat catccattg                                              19


<210>  11
<211>  19
<212>  DNA
<213>  Artificial

<220>
<223>  An artificial synthesized target sequence for siRNA

<400>  11
gaagcagcac gacttcttc                                              19


<210>  12
<211>  51
<212>  DNA
<213>  Artificial

<220>
<223>  An artificially synthesized sequence for siRNA

<400>  12
```

```
caccgcagca ccatcatcca ttgttcaaga gacaatggat gatggtgctg c          51


<210>  13
<211>  51
<212>  DNA
<213>  Artificial


<220>
<223>  An artificially synthesized sequence for siRNA

<400>  13
aaaagcagca ccatcatcca ttgtctcttg aacaatggat gatggtgctg c          51


<210>  14
<211>  47
<212>  DNA
<213>  Artificial


<220>
<223>  siRNA hairpin design

<400>  14
gcagcaccat catccattgt tcaagagaca atggatgatg gtgctgc              47


<210>  15
<211>  4863
<212>  DNA
<213>  Artificial


<220>
<223>  An artificially constructed plasmid sequence of siRNA  expression
       vector.

<400>  15
gacggatcgg gagatctccc gatcccctat ggtgcactct cagtacaatc tgctctggat    60
ccactagtaa cggccgccag tgtgctggaa ttcggcttgg ggatcagcgt ttgagtaaga   120
gcccgcgtct gaaccctccg cgccgccccg gccccagtgg aaagacgcgc aggcaaaacg   180
caccacgtga cggagcgtga ccgcgcgccg agcgcgcgcc aaggtcgggc aggaagaggg   240
cctatttccc atgattcctt catatttgca tatacgatac aaggctgtta gagagataat   300
tagaattaat ttgactgtaa acacaaagat attagtacaa aatacgtgac gtagaaagta   360
ataatttctt gggtagtttg cagttttaaa attatgtttt aaaatggact atcatatgct   420
taccgtaact tgaaagtatt tcgatttctt ggctttatat atcttgtgga aggacgaaa    480
cacctttta catcaggttg ttttttctgtt tggttttttt tttacaccac gtttatacgc   540
cggtgcacgg tttaccactg aaaacacctt tcatctacag gtgatatctt ttaacacaaa   600
taaaatgtag tagtcctagg agacggaata gaaggaggtg gggcctaaag ccgaattctg   660
cagatatcca tcacactggc ggccgctcga gtgaggcgga agaaccagc tggggctcta   720
gggggtatcc ccacgcgccc tgtagcggcg cattaagcgc ggcgggtgtg gtggttacgc   780
gcagcgtgac cgctacactt gccagcgccc tagcgcccgc tcctttcgct ttcttccctt   840
cctttctcgc cacgttcgcc ggctttcccc gtcaagctct aaatcggggg ctccctttag   900
ggttccgatt tagtgcttta cggcacctcg accccaaaaa acttgattag ggtgatggtt   960
cacgtagtgg gccatcgccc tgatagacgg ttttttcgccc tttgacgttg gagtccacgt  1020
tctttaatag tggactcttg ttccaaactg gaacaacact caaccctatc tcggtctatt  1080
cttttgattt ataagggatt ttgccgattt cggcctattg gttaaaaaat gagctgattt  1140
aacaaaaatt taacgcgaat taattctgtg gaatgtgtgt cagttagggt gtggaaagtc  1200
cccaggctcc ccagcaggca gaagtatgca aagcatgcat ctcaattagt cagcaaccag  1260
gtgtggaaag tccccaggct ccccagcagg cagaagtatg caaagcatgc atctcaatta  1320
gtcagcaacc atagtcccgc ccctaactcc gcccatcccg cccctaactc cgcccagttc  1380
cgcccattct ccgccccatg ctgactaat tttttttatt tatgcagagg ccgaggccgc  1440
```

                                  11

```
ctctgcctct gagctattcc agaagtagtg aggaggcttt tttggaggcc taggcttttg   1500
caaaaagctc ccgggagctt gtatatccat tttcggatct gatcaagaga caggatgagg   1560
atcgtttcgc atgattgaac aagatggatt gcacgcaggt tctccggccg cttgggtgga   1620
gaggctattc ggctatgact gggcacaaca gacaatcggc tgctctgatg ccgccgtgtt   1680
ccggctgtca gcgcagggggc gcccggttct ttttgtcaag accgacctgt ccggtgccct   1740
gaatgaactg caggacgagg cagcgcggct atcgtggctg gccacgacgg gcgttccttg   1800
cgcagctgtg ctcgacgttg tcactgaagc gggaagggac tggctgctat tgggcgaagt   1860
gccggggcag gatctcctgt catctcacct tgctcctgcc gagaaagtat ccatcatggc   1920
tgatgcaatg cggcggctgc atacgcttga tccggctacc tgcccattcg accaccaagc   1980
gaaacatcgc atcgagcgag cacgtactcg gatggaagcc ggtcttgtcg atcaggatga   2040
tctggacgaa gagcatcagg ggctcgcgcc agccgaactg ttcgccaggc tcaaggcgcg   2100
catgcccgac ggcgaggatc tcgtcgtgac ccatggcgat gcctgcttgc cgaatatcat   2160
ggtggaaaat ggccgctttt ctggattcat cgactgtggc cggctgggtg tggcggaccg   2220
ctatcaggac atagcgttgg ctacccgtga tattgctgaa gagcttggcg gcgaatgggc   2280
tgaccgcttc ctcgtgcttt acggtatcgc cgctcccgat tcgcagcgca tcgccttcta   2340
tcgccttctt gacgagttct tctgagcggg actctggggt tcgaaatgac cgaccaagcg   2400
acgcccaacc tgccatcacg agatttcgat tccaccgccg ccttctatga aaggttgggc   2460
ttcggaatcg ttttccggga cgccggctgg atgatcctcc agcgcgggga tctcatgctg   2520
gagttcttcg cccaccccaa cttgtttatt gcagcttata atggttacaa ataaagcaat   2580
agcatcacaa atttcacaaa taaagcattt ttttcactgc attctagttg tggtttgtcc   2640
aaactcatca atgtatctta tcatgtctgt ataccgtcga cctctagcta gagcttggcg   2700
taatcatggt catagctgtt tcctgtgtga aattgttatc cgctcacaat tccacacaac   2760
atacgagccg gaagcataaa gtgtaaagcc tggggtgcct aatgagtgag ctaactcaca   2820
ttaattgcgt tgcgctcact gcccgctttc cagtcgggaa acctgtcgtg ccagctgcat   2880
taatgaatcg gccaacgcgc ggggagaggc ggtttgcgta ttgggcgctc ttccgcttcc   2940
tcgctcactg actcgctgcg ctcggtcgtt cggctgcggc gagcggtatc agctcactca   3000
aaggcggtaa tacggttatc cacagaatca ggggataacg caggaaagaa catgtgagca   3060
aaaggccagc aaaaggccag gaaccgtaaa aaggccgcgt tgctggcgtt tttccatagg   3120
ctccgccccc ctgacgagca tcacaaaaat cgacgctcaa gtcagaggtg gcgaaacccg   3180
acaggactat aaagatacca ggcgtttccc cctggaagct ccctcgtgcg ctctcctgtt   3240
ccgaccctgc cgcttaccgg atacctgtcc gcctttctcc cttcgggaag cgtggcgctt   3300
tctcatagct cacgctgtag gtatctcagt tcggtgtagg tcgttcgctc caagctgggc   3360
tgtgtgcacg aaccccccgt tcagcccgac cgctgcgcct tatccggtaa ctatcgtctt   3420
gagtccaacc cggtaagaca cgacttatcg ccactggcag cagccactgg taacaggatt   3480
agcagagcga ggtatgtagg cggtgctaca gagttcttga agtggtggcc taactacggc   3540
tacactagaa gaacagtatt tggtatctgc gctctgctga agccagttac cttcggaaaa   3600
agagttggta gctcttgatc cggcaaacaa accaccgctg gtagcggttt ttttgtttgc   3660
aagcagcaga ttacgcgcag aaaaaaagga tctcaagaag atcctttgat cttttctacg   3720
gggtctgacg ctcagtggaa cgaaaactca cgttaaggga ttttggtcat gagattatca   3780
aaaaggatct tcacctagat ccttttaaat taaaaatgaa gttttaaatc aatctaaagt   3840
atatatgagt aaacttggtc tgacagttac caatgcttaa tcagtgaggc acctatctca   3900
gcgatctgtc tatttcgttc atccatagtt gcctgactcc ccgtcgtgta gataactacg   3960
atacgggagg gcttaccatc tggccccagt gctgcaatga taccgcgaga cccacgctca   4020
ccggctccag atttatcagc aataaaccag ccagccggaa gggccgagcg cagaagtggt   4080
cctgcaactt tatccgcctc catccagtct attaattgtt gccgggaagc tagagtaagt   4140
agttcgccag ttaatagttt gcgcaacgtt gttgccattg ctacaggcat cgtggtgtca   4200
cgctcgtcgt ttggtatggc ttcattcagc tccggttccc aacgatcaag gcgagttaca   4260
tgatccccca tgttgtgcaa aaaagcggtt agctccttcg gtcctccgat cgttgtcaga   4320
agtaagttgg ccgcagtgtt atcactcatg gttatggcag cactgcataa ttctcttact   4380
gtcatgccat ccgtaagatg cttttctgtg actggtgagt actcaaccaa gtcattctga   4440
gaatagtgta tgcggcgacc gagttgctct tgcccggcgt caatacggga taataccgcg   4500
ccacatagca gaactttaaa agtgctcatc attggaaaac gttcttcggg gcgaaaactc   4560
tcaaggatct taccgctgtt gagatccagt tcgatgtaac ccactcgtgc acccaactga   4620
tcttcagcat cttttacttt caccagcgtt tctgggtgag caaaaacagg aaggcaaaat   4680
gccgcaaaaa agggaataag ggcgacacgg aaatgttgaa tactcatact cttcctttt   4740
caatattatt gaagcattta tcagggttat tgtctcatga gcggatacat atttgaatgt   4800
atttagaaaa ataaacaaat aggggttccg cgcacatttc cccgaaaagt gccacctgac   4860
gtc                                                                4863
```

<210> 16
```

12

```
<211>   20
<212>   DNA
<213>   artificial

<220>
<223>   An artificially synthesized primer sequence

<400>   16
ggggatcagc gtttgagtaa                                                    20


<210>   17
<211>   20
<212>   DNA
<213>   artificial

<220>
<223>   An artificially synthesized primer sequence

<400>   17
taggccccac ctccttctat                                                    20


<210>   18
<211>   30
<212>   DNA
<213>   artificial

<220>
<223>   An artificially synthesized primer sequence

<400>   18
tgcggatcca gagcagattg tactgagagt                                         30


<210>   19
<211>   29
<212>   DNA
<213>   artificial

<220>
<223>   An artificially synthesized primer sequence

<400>   19
ctctatctcg agtgaggcgg aaagaacca                                          29


<210>   20
<211>   40
<212>   DNA
<213>   artificial

<220>
<223>   An artificially synthesized primer sequence

<400>   20
tttaagcttg aagactattt ttacatcagg ttgtttttct                              40


<210>   21
<211>   37
```

```
<212>   DNA
<213>   artificial

<220>
<223>   An artificially synthesized primer sequence

<400>   21
tttaagcttg aagacacggt gtttcgtcct ttccaca                                37


<210>   22
<211>   51
<212>   DNA
<213>   artificial

<220>
<223>   An artificially synthesized sequence for siRNA

<400>   22
caccgaagca gcacgacttc ttcttcaaga gagaagaagt cgtgctgctt c               51


<210>   23
<211>   51
<212>   DNA
<213>   artificial

<220>
<223>   An artificially synthesized sequence for siRNA

<400>   23
aaaagaagca gcacgacttc ttctctcttg aagaagaagt cgtgctgctt c               51
```